



741179.ST25.txt  
SEQUENCE LISTING

<110> Wang, Jin-Town  
Lin, Tzu-Lung

<120> A TYPE II RESTRICTION ENDONUCLEASE AND APPLICATION THEREOF

<130> P/741-179

<140> 10/796,669  
<141> 2004-03-09

<160> 5

<170> PatentIn version 3.2

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<213> Helicobacter pylori

<400> 1

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48

cga aac cct aaa aga ata gga caa ttt tta gct gtt tta gga aag ttt  
Arg Asn Pro Lys Arg Ile Gly Gln Phe Leu Ala Val Leu Gly Lys Phe  
20 25 30

96

gaa aat caa atc ctt aaa tct tca ata atc atg caa att atc aaa tcc  
Glu Asn Gln Ile Leu Lys Ser Ser Ile Ile Met Gln Ile Ile Lys Ser  
35 40 45

144

gtt ttg gct cat agg ctt tat aga cct act tct ctc aat caa aat aaa  
Val Leu Ala His Arg Leu Tyr Arg Pro Thr Ser Leu Asn Gln Asn Lys  
50 55 60

192

gaa ttg aaa gaa aaa ttt gac tcc aat gaa tat gtc ttt agc gat gaa  
Glu Leu Lys Glu Lys Phe Asp Ser Asn Glu Tyr Val Phe Ser Asp Glu  
65 70 75 80

240

gag tta gaa cgc att ata gaa ata tcc cca caa aat cat aaa gaa atg  
Glu Leu Glu Arg Ile Ile Glu Ile Ser Pro Gln Asn His Lys Glu Met  
85 90 95

288

ggc ttt gag cat gga tgg gaa agc cgg ttt gac act tgg tat aag ctt  
Gly Phe Glu His Gly Trp Glu Ser Arg Phe Asp Thr Trp Tyr Lys Leu  
100 105 110

336

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atg tgt gag ttt ggt ttt tgc tac tat gca aaa tat gag aaa ata ctc Met Cys Glu Phe Gly Phe Cys Tyr Tyr Ala Lys Tyr Glu Lys Ile Leu 115 120 125	384
atc agc gat agc gct aag atg ctt att ctt gct tat tac aat aaa gaa Ile Ser Asp Ser Ala Lys Met Leu Ile Leu Ala Tyr Tyr Asn Lys Glu 130 135 140	432
aac gat gct ttt aaa gaa agc gtt gat gaa agc gta gtt ggg gct ata Asn Asp Ala Phe Lys Glu Ser Val Asp Glu Ser Val Val Gly Ala Ile 145 150 155 160	480
ttt tta aac gct ctg tct aaa tat gaa gta gga aac cct tac aaa aag Phe Leu Asn Ala Leu Ser Lys Tyr Glu Val Gly Asn Pro Tyr Lys Lys 165 170 175	528
aat tta aac cat aac aac cct ttc aaa cta ttg ctc tcg ctt tta aaa Asn Leu Asn His Asn Asn Pro Phe Lys Leu Leu Leu Ser Leu Leu Lys 180 185 190	576
cga ctc aaa aat gcc cat cta acc ccc cta tct gtc aaa gaa atc cct Arg Leu Lys Asn Ala His Leu Thr Pro Leu Ser Val Lys Glu Ile Pro 195 200 205	624
att tta ctt tgt tgg aaa gac gat aac gct aat ggg ctt tat gac tac Ile Leu Leu Cys Trp Lys Asp Asp Asn Ala Asn Gly Leu Tyr Asp Tyr 210 215 220	672
att att cgt tta aga caa gaa atc gtt act atc aat aaa aca gaa ttc Ile Ile Arg Leu Arg Gln Glu Ile Val Thr Ile Asn Lys Thr Glu Phe 225 230 235 240	720
agc tac tca gat gaa ttt atc tat gaa aaa tgc cta aaa ctt tta gaa Ser Tyr Ser Asp Glu Phe Ile Tyr Glu Lys Cys Leu Lys Leu Leu Glu 245 250 255	768
agt gtt aat aaa aca cga ttt aaa atg agc caa atc act aac gaa gcc Ser Val Asn Lys Thr Arg Phe Lys Met Ser Gln Ile Thr Asn Glu Ala 260 265 270	816
gtt gat gaa tac att aga aaa atg cgt att aca gga ctt att tca ttg Val Asp Glu Tyr Ile Arg Lys Met Arg Ile Thr Gly Leu Ile Ser Leu 275 280 285	864
cgt ggt aat ggt agg ttt att gat att aat act aat gaa aat aat aaa Arg Gly Asn Gly Arg Phe Ile Asp Ile Asn Thr Asn Glu Asn Asn Lys 290 295 300	912
ata gat tac att tta caa acc cat aag gct ttt aaa ggg gat tat tta Ile Asp Tyr Ile Leu Gln Thr His Lys Ala Phe Lys Gly Asp Tyr Leu 305 310 315 320	960
aac gac act caa gct aac aaa ctc gcc ttt ttt aac tac atg gcg atc Asn Asp Thr Gln Ala Asn Lys Leu Ala Phe Phe Asn Tyr Met Ala Ile 325 330 335	1008
gtg gat agc ttt ctt gtt agt gtt act cca atc agc gct aat gag agc Val Asp Ser Phe Leu Val Ser Val Thr Pro Ile Ser Ala Asn Glu Ser 340 345 350	1056
gtt aaa tca agc aaa ttg aat gaa cta gca aac act tat act aaa gat Val Lys Ser Ser Lys Leu Asn Glu Leu Ala Asn Thr Tyr Thr Lys Asp	1104

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355	360	365	
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gat agt ttt tta aga ctc att gat aaa cct tta cgc tta gaa ttt tta Asp Ser Phe Leu Arg Leu Ile Asp Lys Pro Leu Arg Leu Glu Phe Leu 385 390 395 400			1200
agc gct att ttc ttg aaa caa cat ttt gaa aat tta agc gtg ata ccc Ser Ala Ile Phe Leu Lys Gln His Phe Glu Asn Leu Ser Val Ile Pro 405 410 415			1248
aat tat aaa agc gat gat gaa ggc ttg ccc gta tac aca gca agc ggt Asn Tyr Lys Ser Asp Asp Glu Gly Leu Pro Val Tyr Thr Ala Ser Gly 420 425 430			1296
aat aaa cct gat att gta gct atg gac aca aaa gcc caa agt tat ata Asn Lys Pro Asp Ile Val Ala Met Asp Thr Lys Ala Gln Ser Tyr Ile 435 440 445			1344
gaa gtg agc ttg att aga gac aga agt caa agt acc ttg gaa atg ata Glu Val Ser Leu Ile Arg Asp Arg Ser Gln Ser Thr Leu Glu Met Ile 450 455 460			1392
cct att gcc aga cat tta aaa gaa ttg att aaa aat agc acc gat att Pro Ile Ala Arg His Leu Lys Glu Leu Ile Lys Asn Ser Thr Asp Ile 465 470 475 480			1440
aga gaa aaa ttt agt gtt ttt gta gct cca aat atc cat gat gat gcc Arg Glu Lys Phe Ser Val Phe Val Ala Pro Asn Ile His Asp Asp Ala 485 490 495			1488
aaa gaa tat gcg gaa ttt gcc caa ttc aaa gac aat att aat ata tgt Lys Glu Tyr Ala Glu Phe Ala Gln Phe Lys Asp Asn Ile Asn Ile Cys 500 505 510			1536
tgt tat gct att aat gat ttt atc aaa aaa gta gaa aac agc ata gaa Cys Tyr Ala Ile Asn Asp Phe Ile Lys Lys Val Glu Asn Ser Ile Glu 515 520 525			1584
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 <212> PRT  
 <213> Helicobacter pylori

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20 25 30

Glu Asn Gln Ile Leu Lys Ser Ser Ile Ile Met Gln Ile Ile Lys Ser  
Page 3

35

40

45

Val Leu Ala His Arg Leu Tyr Arg Pro Thr Ser Leu Asn Gln Asn Lys  
 50 55 60

Glu Leu Lys Glu Lys Phe Asp Ser Asn Glu Tyr Val Phe Ser Asp Glu  
 65 70 75 80

Glu Leu Glu Arg Ile Ile Glu Ile Ser Pro Gln Asn His Lys Glu Met  
 85 90 95

Gly Phe Glu His Gly Trp Glu Ser Arg Phe Asp Thr Trp Tyr Lys Leu  
 100 105 110

Met Cys Glu Phe Gly Phe Cys Tyr Tyr Ala Lys Tyr Glu Lys Ile Leu  
 115 120 125

Ile Ser Asp Ser Ala Lys Met Leu Ile Leu Ala Tyr Tyr Asn Lys Glu  
 130 135 140

Asn Asp Ala Phe Lys Glu Ser Val Asp Glu Ser Val Val Gly Ala Ile  
 145 150 155 160

Phe Leu Asn Ala Leu Ser Lys Tyr Glu Val Gly Asn Pro Tyr Lys Lys  
 165 170 175

Asn Leu Asn His Asn Asn Pro Phe Lys Leu Leu Leu Ser Leu Leu Lys  
 180 185 190

Arg Leu Lys Asn Ala His Leu Thr Pro Leu Ser Val Lys Glu Ile Pro  
 195 200 205

Ile Leu Leu Cys Trp Lys Asp Asp Asn Ala Asn Gly Leu Tyr Asp Tyr  
 210 215 220

Ile Ile Arg Leu Arg Gln Glu Ile Val Thr Ile Asn Lys Thr Glu Phe  
 225 230 235 240

Ser Tyr Ser Asp Glu Phe Ile Tyr Glu Lys Cys Leu Lys Leu Glu  
 245 250 255

Ser Val Asn Lys Thr Arg Phe Lys Met Ser Gln Ile Thr Asn Glu Ala  
 260 265 270

Val Asp Glu Tyr Ile Arg Lys Met Arg Ile Thr Gly Leu Ile Ser Leu  
 275 280 285

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Arg Gly Asn Gly Arg Phe Ile Asp Ile Asn Thr Asn Glu Asn Asn Lys  
 290 295 300  
  
 Ile Asp Tyr Ile Leu Gln Thr His Lys Ala Phe Lys Gly Asp Tyr Leu  
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 Asn Asp Thr Gln Ala Asn Lys Leu Ala Phe Phe Asn Tyr Met Ala Ile  
 325 330 335  
  
 Val Asp Ser Phe Leu Val Ser Val Thr Pro Ile Ser Ala Asn Glu Ser  
 340 345 350  
  
 Val Lys Ser Ser Lys Leu Asn Glu Leu Ala Asn Thr Tyr Thr Lys Asp  
 355 360 365  
  
 Phe Ile Lys Gln Glu Leu Leu Ile Thr Cys Asn Lys Gln Glu Ser Lys  
 370 375 380  
  
 Asp Ser Phe Leu Arg Leu Ile Asp Lys Pro Leu Arg Leu Glu Phe Leu  
 385 390 395 400  
  
 Ser Ala Ile Phe Leu Lys Gln His Phe Glu Asn Leu Ser Val Ile Pro  
 405 410 415  
  
 Asn Tyr Lys Ser Asp Asp Glu Gly Leu Pro Val Tyr Thr Ala Ser Gly  
 420 425 430  
  
 Asn Lys Pro Asp Ile Val Ala Met Asp Thr Lys Ala Gln Ser Tyr Ile  
 435 440 445  
  
 Glu Val Ser Leu Ile Arg Asp Arg Ser Gln Ser Thr Leu Glu Met Ile  
 450 455 460  
  
 Pro Ile Ala Arg His Leu Lys Glu Leu Ile Lys Asn Ser Thr Asp Ile  
 465 470 475 480  
  
 Arg Glu Lys Phe Ser Val Phe Val Ala Pro Asn Ile His Asp Asp Ala  
 485 490 495  
  
 Lys Glu Tyr Ala Glu Phe Ala Gln Phe Lys Asp Asn Ile Asn Ile Cys  
 500 505 510  
  
 Cys Tyr Ala Ile Asn Asp Phe Ile Lys Lys Val Glu Asn Ser Ile Glu  
 515 520 525  
  
 Trp Leu Gln Ile Asn Asp His Leu Lys Ala  
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ttt aat caa gct tta aag cta gaa gaa aat tat ttt agc caa cat ttt		96
Phe Asn Gln Ala Leu Lys Leu Glu Glu Asn Tyr Phe Ser Gln His Phe		
20 25 30		
agc aac aag ttt ttc agc tat aaa gat tgt gtc aaa atc ggt agc att		144
Ser Asn Lys Phe Phe Ser Tyr Lys Asp Cys Val Lys Ile Gly Ser Ile		
35 40 45		
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Arg Glu His Ile Glu Ser Leu Asn Leu Asp Lys Leu Asn Lys Asp Ile		
50 55 60		
tta tta aca agc ctg att tat tca atg gat aag ata gct aac acg gta		240
Leu Leu Thr Ser Leu Ile Tyr Ser Met Asp Lys Ile Ala Asn Thr Val		
65 70 75 80		
ggg cat tat gaa gct tat agg aaa aaa gag att ttg caa gat aga ttt		288
Gly His Tyr Glu Ala Tyr Arg Lys Lys Glu Ile Leu Gln Asp Arg Phe		
85 90 95		
att ttt gag ctt att agc cct ata aaa cat gat aaa aat atc atg ata		336
Ile Phe Glu Leu Ile Ser Pro Ile Lys His Asp Lys Asn Ile Met Ile		
100 105 110		
gag aga aaa aac gct aac gaa ttg gct aaa acc tta aaa ata gac tta		384
Glu Arg Lys Asn Ala Asn Glu Leu Ala Lys Thr Leu Lys Ile Asp Leu		
115 120 125		
gtc ttt att gat cct cca tac aat tca agg caa tac agc cgg ttt tat		432
Val Phe Ile Asp Pro Pro Tyr Asn Ser Arg Gln Tyr Ser Arg Phe Tyr		
130 135 140		
cat ctc tat gaa aac cta gtg cag tgg aaa aaa ccc aaa ctc tat gga		480
His Leu Tyr Glu Asn Leu Val Gln Trp Lys Lys Pro Lys Leu Tyr Gly		
145 150 155 160		
aca gct tta aag cca tca tgc gag aac atg agc gaa tat tgc cgc tct		528
Thr Ala Leu Lys Pro Ser Cys Glu Asn Met Ser Glu Tyr Cys Arg Ser		
165 170 175		
aat gcc aag aaa gaa ttg agc gat tta att gaa aaa cta gat tgt aaa		576
Asn Ala Lys Lys Glu Leu Ser Asp Leu Ile Glu Lys Leu Asp Cys Lys		
180 185 190		
agg att gct tta act tat aat aat acc tat aac tct aag tct agc tct		624
Arg Ile Ala Leu Thr Tyr Asn Asn Thr Tyr Asn Ser Lys Ser Ser Ser		
195 200 205		

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tcg caa aat aaa ata ggc ttt aaa gat tta gtg gaa att ttg agt caa 672  
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 210 215 220

aaa gga aaa tta agc gtt aaa gaa aag gct cat agt ttt ttt aat tca 720  
 Lys Gly Lys Leu Ser Val Lys Glu Lys Ala His Ser Phe Phe Asn Ser  
 225 230 235 240

gga aaa act gat ttt aaa gag cat aaa gaa ttt tta ttt ata gtg gaa 768  
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 245 250 255

gtg aaa cct tga 780  
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gag cct ttt gtg ggt ggg ggt agc gtg ttt tta aac act aag gct aag 96  
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 20 25 30

aga tac tta gct aat gac ata gat act aat att atc aat tta cat aaa 144  
 Arg Tyr Leu Ala Asn Asp Ile Asp Thr Asn Ile Ile Asn Leu His Lys  
 35 40 45

act tta agc aag ttc aat gtt tgt gag ctt ttt gat gaa ttg tct aaa 192  
 Thr Leu Ser Lys Phe Asn Val Cys Glu Leu Phe Asp Glu Leu Ser Lys  
 50 55 60

att atc att cat tat ggc ttg tct ttc tct ttt aag ggg att atg gcc 240  
 Ile Ile Ile His Tyr Gly Leu Ser Phe Ser Phe Lys Gly Ile Met Ala  
 65 70 75 80

cct gat gaa tta aaa aaa caa tat ata aaa act tac tac gcc aaa tac 288  
 Pro Asp Glu Leu Lys Lys Gln Tyr Ile Lys Thr Tyr Tyr Ala Lys Tyr  
 85 90 95

aat aaa ata gct tat gaa aaa cta agg gct gat ttt aac tcc aat caa 336  
 Asn Lys Ile Ala Tyr Glu Lys Leu Arg Ala Asp Phe Asn Ser Asn Gln  
 100 105 110

aac aac atg ctt tat ttg tat ttg ctt tta att tat gga ttt aat cac 384  
 Asn Asn Met Leu Tyr Leu Tyr Leu Leu Leu Ile Tyr Gly Phe Asn His  
 115 120 125

atg att aga ttt aat tct aaa ggg ctt ttt aat tta cct gtg ggt aat 432  
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 130 135 140

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145 150 155 160	
ttt ata cag caa aac acc att att ttt cac aat gat gat tat att gat	528
Phe Ile Gln Gln Asn Thr Ile Ile Phe His Asn Asp Asp Tyr Ile Asp	
165 170 175	
ttt ctt aac cac acc act tat tta aaa gat gat tat gtt tat ttt gac	576
Phe Leu Asn His Thr Thr Tyr Leu Lys Asp Asp Tyr Val Tyr Phe Asp	
180 185 190	
ccc cct tat tta atc tcc aat agt gaa tac aac aag tta tgg gat agc	624
Pro Pro Tyr Leu Ile Ser Asn Ser Glu Tyr Asn Lys Leu Trp Asp Ser	
195 200 205	
gat aat gag ata gcc tta tat ggt gtt tta gat agc cta gat aaa aag	672
Asp Asn Glu Ile Ala Leu Tyr Gly Val Leu Asp Ser Leu Asp Lys Lys	
210 215 220	
gga gtt tta ttt ggt ata act aat ctt att tat cac aag gga gag act	720
Gly Val Leu Phe Gly Ile Thr Asn Leu Ile Tyr His Lys Gly Glu Thr	
225 230 235 240	
aat ttt att tta aaa gaa tgg gct aaa aaa tat tat att ttt aat atc	768
Asn Phe Ile Leu Lys Glu Trp Ala Lys Lys Tyr Tyr Ile Phe Asn Ile	
245 250 255	
aaa agt aat tat atc agt tat aat gac aat act att aaa gaa gat agt	816
Lys Ser Asn Tyr Ile Ser Tyr Asn Asp Asn Thr Ile Lys Glu Asp Ser	
260 265 270	
caa gaa atc ttt gta act aat tat agg tga	846
Gln Glu Ile Phe Val Thr Asn Tyr Arg	
275 280	